

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMM file: /data/isb2k/blastdb/Pfam72/Pfam72

Sequence file: /u/legal/jennyb/pf619.seq

Query: 4325626CD1

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
TBC	TBC domain	33.3	9.9e-10	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
TBC	1/1	98	315	1	341	33.3	9.9e-10

Alignments of top-scoring domains:

TBC: domain 1 of 1, from 98 to 315: score 33.3, E = 9.9e-10

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      *->vrqgvpslRgkVWkl1lgagelnnc1ltdnfnkgldlfglvpl1lla
          +g p + Rg W +11++ e+                      +1+
4325626CD1  98  AYKGMPMNIRGPMWSVLLNTEEM-----KLK 123

      dkdeYeellnknkektvqdqneKssvgirrldyVEAVEKHPLSDDNDKTK
      +++++Y+  +k+k +  +
4325626CD1  124 NPGRYQIMKEKGKRSEH----- 141

      GSLekgsdekalklredldkIekDlsRTfpdeiffqtrlaeqqlkkdqdl
          +++I++D+s T+++ iff+ r
4325626CD1  142 -----IQRIDRDVSGTLRKHIFFRDR----- 162

      daydkDEfddeddkneppsikqLrrlLvaYswknpqehlgYvQGMnvils
          +  ++ L  +L aY  +np  +gY+  + i++
4325626CD1  163 -----YGTKQRELLHILLAYEEYNPE--VGYCRDLSHIAA 195

      pLLlflkhgvdldedeeqAFwclvkLm..dnylpqkyflndlsghnedl
      ++Ll l          +ee+AFw+lv L+ +++  +q +++++  +++  +
4325626CD1  196 LFLLYL-----PEEDAFWALVQLLasERHSLQGFHSPNGGTVQGLQ 236

      rvLdslvkeslPeLyshlkkkenktgsgkKknllaldltllifafpwlTt
          + ++ v s P+  h kk                      +  ++ +  +++
4325626CD1  237 DQQEHVVATSQPKTMGHQDKK-----DLCGQCSPLGCLIRI 272

      lFarelPleivlrIwDilftyYlgshflifvalAiLkllkskllkh<-*
      l ++  +l  +lr+wD+++  + g + l  +          +k + l k
4325626CD1  273 L-IDGISLGLTLRLWDVYLVE--GEQALMPITRIAFKVQKRLTKT 315

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